

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1275

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC	48
	Met Val Glu Met Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
	1 5 10 15	
25	TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC	96
	Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
	20 25 30	
30	ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG	144
	Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
35	CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
	50 55 60	
40	TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
	65 70 75 80	
	CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
	85 90 95	
45	GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG	336
	Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
	100 105 110	
50	GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC	384
	Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	
55	GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC	432
	Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
	130 135 140	
60	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
	145 150 155 160	

	TAC Tyr	GGA Gly	ATG Met	CTG Leu	GCC Ala 165	CGC Arg	CTC Leu	GCC Ala	GTC Val	GAG Glu 170	GCC Ala	GGC Gly	TTC Phe	GAC Asp	TGG Trp 175	GTC Val	528
5	TAC Tyr	TAC Tyr	GAG Glu	TCC Ser 180	AAG Lys	GCG Ala	CAC His	ATC Ile	CAC His 185	TGC Cys	TCC Ser	GTC Val	AAA Lys	GCA Ala 190	GAA Glu	AAC Asn	576
10	TCA Ser	GTG Val	GCA Ala 195	GCG Ala	AAA Lys	TCA Ser	GGA Gly	GGC Gly 200	TGC Cys	TTC Phe	CCT Pro	GGC Gly	TCA Ser 205	GCC Ala	ACA Thr	GTG Val	624
15	CAC His	CTG Leu 210	GAG Glu	CAT His	GGA Gly	GGC Gly	ACC Thr 215	AAG Lys	CTG Leu	GTG Val	AAG Lys	GAC Asp 220	CTG Leu	AGC Ser	CCT Pro	GGG Gly	672
20	GAC Asp 225	CGC Arg	GTG Val	CTG Leu	GCT Ala 230	GCT Ala	GAC Asp	GCG Ala	GAC Asp	GGC Gly	CGG Arg 235	CTG Leu	CTC Leu	TAC Tyr	AGT Ser	GAC Asp 240	720
	TTC Phe	CTC Leu	ACC Thr	TTC Phe	CTC Leu 245	GAC Asp	CGG Arg	ATG Met	GAC Asp	AGC Ser 250	TCC Ser	CGA Arg	AAG Lys	CTC Leu	TTC Phe 255	TAC Tyr	768
25	GTC Val	ATC Ile	GAG Glu	ACG Thr 260	CGG Arg	CAG Gln	CCC Pro	CGG Arg	GCC Ala 265	CGG Arg	CTG Leu	CTA Leu	CTG Leu	ACG Thr 270	GCG Ala	GCC Ala	816
30	CAC His	CTG Leu	CTC Leu 275	TTT Phe	GTG Val	GCC Ala	CCC Pro	CAG Gln 280	CAC His	AAC Asn	CAG Gln	TCG Ser	GAG Glu 285	GCC Ala	ACA Thr	GGG Gly	864
35	TCC Ser	ACC Thr 290	AGT Ser	GGC Gly	CAG Gln	GCG Ala	CTC Leu 295	TTC Phe	GCC Ala	AGC Ser	AAC Asn	GTG Val 300	AAG Lys	CCT Pro	GGC Gly	CAA Gln	912
40	CGT Arg 305	GTC Val	TAT Tyr	GTG Val	CTG Leu	GGC Gly 310	GAG Glu	GGC Gly	GGG Gly	CAG Gln	CAG Gln 315	CTG Leu	CTG Leu	CCG Pro	GCG Ala	TCT Ser 320	960
	GTC Val	CAC His	AGC Ser	GTC Val	TCA Ser 325	TTG Leu	CGG Arg	GAG Glu	GAG Glu	GCG Ala 330	TCC Ser	GGA Gly	GCC Ala	TAC Tyr	GCC Ala 335	CCA Pro	1008
45	CTC Leu	ACC Thr	GCC Ala	CAG Gln 340	GGC Gly	ACC Thr	ATC Ile	CTC Leu	ATC Ile 345	AAC Asn	CGG Arg	GTG Val	TTG Leu	GCC Ala 350	TCC Ser	TGC Cys	1056
50	TAC Tyr	GCC Ala	GTC Val 355	ATC Ile	GAG Glu	GAG Glu	CAC His	AGT Ser 360	TGG Trp	GCC Ala	CAT His	TGG Trp	GCC Ala 365	TTC Phe	GCA Ala	CCA Pro	1104
55	TTC Phe	CGC Arg 370	TTG Leu	GCT Ala	CAG Gln	GGG Gly	CTG Leu 375	CTG Leu	GCC Ala	GCC Ala	CTC Leu	TGC Cys 380	CCA Pro	GAT Asp	GGG Gly	GCC Ala	1152
	ATC Ile 385	CCT Pro	ACT Thr	GCC Ala	GCC Ala	ACC Thr 390	ACC Thr	ACC Thr	ACT Thr	GGC Gly 395	ATC Ile	CAT His	TGG Trp	TAC Tyr	TCA Ser	CGG Arg 400	1200
60	CTC Leu	CTC Leu	TAC Tyr	CGC Arg	ATC Ile	GGC Gly	AGC Ser	TGG Trp	GTG Val	CTG Leu	GAT Asp	GGT Gly	GAC Asp	GCG Ala	CTG Leu	CAT His	1248

415

1277

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TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC 432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140

TABLE OF T2222

5	CGT Arg 145	GCC Ala	TTG Leu	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCT Ser	GAC Asp	CGT Arg	GAC Asp 155	CGT Arg	AAT Asn	AAG Lys	TAT Tyr	GGT Gly 160	480
	TTG Leu	TTG Leu	GCG Ala	CGC Arg	CTA Leu 165	GCT Ala	GTG Val	GAA Glu	GCC Ala	GGA Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAC Tyr	528
10	GAG Glu	TCC Ser	CGC Arg	AAC Asn 180	CAC His	ATC Ile	CAC His	GTA Val	TCG Ser 185	GTC Val	AAA Lys	GCT Ala	GAT Asp	AAC Asn 190	TCA Ser	CTG Leu	576
15	GCG Ala	GTC Val	CGA Arg 195	GCC Ala	GGA Gly	GGC Gly	TGC Cys 200	TTT Phe	CCG Pro	GGA Gly	AAT Asn	GCC Ala	ACG Thr 205	GTG Val	CGC Arg	TTG Leu	624
20	CGG Arg	AGC Ser 210	GGC Gly	GAA Glu	CGG Arg	AAG Lys	GGG Gly 215	CTG Leu	AGG Arg	GAA Glu	CTA Leu	CAT His 220	CGT Arg	GGT Gly	GAC Asp	TGG Trp	672
25	GTA Val 225	CTG Leu	GCC Ala	GCT Ala	GAT Asp	GCA Ala 230	GCG Ala	GGC Gly	CGA Arg	GTG Val	GTA Val 235	CCC Pro	ACG Thr	CCA Pro	GTG Val	CTG Leu 240	720
	CTC Leu	TTC Phe	CTG Leu	GAC Asp	CGG Arg 245	GAT Asp	CTG Leu	CAG Gln	CGC Arg	CGC Arg 250	GCC Ala	TCG Ser	TTC Phe	GTG Val	GCT Ala 255	GTG Val	768
30	GAG Glu	ACC Thr	GAG Glu	CGG Arg 260	CCT Pro	CCG Pro	CGC Arg	AAA Lys	CTG Leu 265	TTG Leu	CTC Leu	ACA Thr	CCC Pro	TGG Trp 270	CAT His	CTG Leu	816
35	GTG Val	TTC Phe 275	GCT Ala	GCT Ala	CGC Arg	GGG Gly	CCA Pro	GCG Ala 280	CCT Pro	GCT Ala	CCA Pro	GGT Gly	GAC Asp 285	TTT Phe	GCA Ala	CCG Pro	864
40	GTG Val 290	TTC Phe	GCG Ala	CGC Arg	CGC Arg	TTA Leu	CGT Arg 295	GCT Ala	GGC Gly	GAC Asp	TCG Ser	GTG Val 300	CTG Leu	GCT Ala	CCC Pro	GGC Gly	912
45	GGG Gly 305	GAC Asp	GCG Ala	CTC Leu	CAG Gln	CCG Pro 310	GCG Ala	CGC Arg	GTA Val	GCC Ala	CGC Arg 315	GTG Val	GCG Ala	CGC Arg	GAG Glu	GAA Glu 320	960
	GCC Ala	GTG Val	GGC Gly	GTG Val	TTC Phe 325	GCA Ala	CCG Pro	CTC Leu	ACT Thr	GCG Ala 330	CAC His	GGG Gly	ACG Thr	CTG Leu 335	CTG Leu	GTC Val	1008
50	AAC Asn	GAC Asp	GTC Val	CTC Leu 340	GCC Ala	TCC Ser	TGC Cys	TAC Tyr	GCG Ala 345	GTT Val	CTA Leu	GAG Glu	AGT Ser	CAC His 350	CAG Gln	TGG Trp	1056
55	GCC Ala	CAC His	CGC Arg 355	GCC Ala	TTC Phe	GCC Ala	CCT Pro	TTG Leu 360	CGG Arg	CTG Leu	CTG Leu	CAC His	GCG Ala 365	CTC Leu	GGG Gly	GCT Ala	1104
60	CTG Leu	CTC Leu 370	CCT Pro	GGG Gly	GGT Gly	GCA Ala	GTC Val 375	CAG Gln	CCG Pro	ACT Thr	GGC Gly	ATG Met 380	CAT His	TGG Trp	TAC Tyr	TCT Ser	1152

1190

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 1..1233
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CCG TTC TGT CTG TTC CTG 48
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG 96
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC 144
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC 192
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG 240
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC 288
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC 336
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG 384
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC TCA GAG GAG TCT TTA 432
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

CAC TAT GAG GGC CGC GCG GTG GAT ATC ACC ACC TCA GAC CGT GAC CGA 480
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg

	145					150					155					160	
5	AAT Asn	AAG Lys	TAT Tyr	GGA Gly	CTG Leu	CTG Leu	GCG Ala	CGC Arg	TTA Leu	GCA Ala	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe	GAC Asp	528
					165					170					175		
10	TGG Trp	GTG Val	TAT Tyr	TAC Tyr	GAG Glu	TCC Ser	AAG Lys	GCC Ala	CAC His	GTG Val	CAT His	TGC Cys	TCT Ser	GTC Val	AAG Lys	TCT Ser	576
				180					185					190			
15	GAG Glu	CAT His	TCG Ser	GCC Ala	GCT Ala	GCC Ala	AAG Lys	ACA Thr	GGT Gly	GGC Gly	TGC Cys	TTT Phe	CCT Pro	GCC Ala	GGA Gly	GCC Ala	624
			195					200					205				
20	CAG Gln	GTG Val	CGC Arg	CTA Leu	GAG Glu	AAC Asn	GGG Gly	GAG Glu	CGT Arg	GTG Val	GCC Ala	CTG Leu	TCA Ser	GCT Ala	GTA Val	AAG Lys	672
		210					215					220					
25	CCA Pro	GGA Gly	GAC Asp	CGG Arg	GTG Val	CTG Leu	GCC Ala	ATG Met	GGG Gly	GAG Glu	GAT Asp	GGG Gly	ACC Thr	CCC Pro	ACC Thr	TTC Phe	720
		225				230				235						240	
30	AGT Ser	GAT Asp	GTG Val	CTT Leu	ATT Ile	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAG Glu	CCA Pro	AAC Asn	CGG Arg	CTG Leu	AGA Arg	GCT Ala	768
				245						250					255		
35	TTC Phe	CAG Gln	GTC Val	ATC Ile	GAG Glu	ACT Thr	CAG Gln	GAT Asp	CCT Pro	CCG Pro	CGT Arg	CGG Arg	CTG Leu	GCG Ala	CTC Leu	ACG Thr	816
				260					265					270			
40	CCT Pro	GCC Ala	CAC His	CTG Leu	CTC Leu	TTC Phe	ATT Ile	GCG Ala	GAC Asp	AAT Asn	CAT His	ACA Thr	GAA Glu	CCA Pro	GCA Ala	GCC Ala	864
			275					280					285				
45	CAC His	TTC Phe	CGG Arg	GCC Ala	ACA Thr	TTT Phe	GCC Ala	AGC Ser	CAT His	GTG Val	CAA Gln	CCA Pro	GGC Gly	CAA Gln	TAT Tyr	GTG Val	912
		290					295					300					
50	CTG Leu	GTA Val	TCA Ser	GGG Gly	GTA Val	CCA Pro	GGC Gly	CTC Leu	CAG Gln	CCT Pro	GCT Ala	CGG Arg	GTG Val	GCA Ala	GCT Ala	GTC Val	960
	305					310				315						320	
55	TCC Ser	ACC Thr	CAC His	GTG Val	GCC Ala	CTT Leu	GGG Gly	TCC Ser	TAT Tyr	GCT Ala	CCT Pro	CTC Leu	ACA Thr	AGG Arg	CAT His	GGG Gly	1008
					325					330					335		
60	ACA Thr	CTT Leu	GTG Val	GTG Val	GAG Glu	GAT Asp	GTG Val	GTG Val	GCC Ala	TCC Ser	TGC Cys	TTT Phe	GCA Ala	GCT Ala	GTG Val	GCT Ala	1056
				340					345				350				
65	GAC Asp	CAC His	CAT His	CTG Leu	GCT Ala	CAG Gln	TTG Leu	GCC Ala	TTC Phe	TGG Trp	CCC Pro	CTG Leu	CGA Arg	CTG Leu	TTT Phe	CCC Pro	1104
			355					360				365					
70	AGT Ser	TTG Leu	GCA Ala	TGG Trp	GGC Gly	AGC Ser	TGG Trp	ACC Thr	CCA Pro	AGT Ser	GAG Glu	GGT Gly	GTT Val	CAC His	TCC Ser	TAC Tyr	1152
		370					375					380					
75	CCT Pro	CAG Gln	ATG Met	CTC Leu	TAC Tyr	CGC Arg	CTG Leu	GGG Gly	CGT Arg	CTC Leu	TTG Leu	CTA Leu	GAA Glu	GAG Glu	AGC Ser	ACC Thr	1200
	385					390				395						400	

CCCTCCTGGA ACTGCTGTGC GTGGATCC 1281

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..1314
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ATG CTG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG 48
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15

CTG	CTG	GTG	TGC	CCC	GGG	CTG	GCC	TGT	GGG	CCC	GGC	AGG	GGG	TTT	GGA	96
Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	
			20					25					30			

AAG AGG CGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT 144
Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45

ATT CCC AAC GTA GCC GAG AAG ACC CTA GGG GCC AGC GGC AGA TAT GAA 192
Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60

GGG AAG ATC ACA AGA AAC TCC GAA CGA TTT AAG GAA CTC ACC CCC AAT 240
Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80

TAC AAC CCC GAC ATC ATA TTT AAG GAT GAG GAA AAC ACG GGA GCA GAC 288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
85 90 95

CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GCC TTG GCC ATC 336
Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
100 105 110

TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC 384
Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT 432
Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
130 135 140

	CGA Arg 145	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCC Ser	GAC Asp	CGG Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly 160	480
5	ATG Met	CTG .Leu	GCT Ala	CGC Arg	CTG Leu 165	GCT Ala	GTG Val	GAA Glu	GCA Ala	GGT Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAT Tyr	528
10	GAA Glu	TCC Ser	AAA Lys	GCT Ala 180	CAC His	ATC Ile	CAC His	TGT Cys	TCT Ser 185	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn 190	TCC Ser	GTG Val	576
15	GCG Ala	GCC Ala	AAA Lys 195	TCC Ser	GGC Gly	GGC Gly	TGT Cys	TTC Phe 200	CCG Pro	GGA Gly	TCC Ser	GCC Ala	ACC Thr 205	GTG Val	CAC His	CTG Leu	624
20	GAG Glu	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu 215	GTG Val	AAG Lys	GAC Asp	TTA Leu 220	CGT Arg	CCC Pro	GGA Gly	GAC Asp	CGC Arg	672
25	GTG Val 225	CTG Leu	GCG Ala	GCT Ala	GAC Asp	GAC Asp 230	CAG Gln	GGC Gly	CGG Arg	CTG Leu	CTG Leu 235	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu 240	720
	ACC Thr	TTC Phe	CTG Leu	GAC Asp	CGC Arg 245	GAC Asp	GAA Glu	GGC Gly	GCC Ala	AAG Lys 250	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val 255	ATC Ile	768
30	GAG Glu	ACG Thr	CTG Leu	GAG Glu 260	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu 265	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	816
35	CTC Leu	TTC Phe	GTG Val 275	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp 280	TCG Ser	GGG Gly	CCC Pro	ACG Thr	CCC Pro 285	GGG Gly	CCA Pro	AGC Ser	864
40	GCG Ala 290	CTC Leu	TTT Phe	GCC Ala	AGC Ser	CGC Arg	GTG Val 295	CGC Arg	CCC Pro	GGG Gly	CAG Gln 300	CGC Arg	GTG Val	TAC Tyr	GTG Val	GTG Val	912
45	GCT Ala 305	GAA Glu	CGC Arg	GGC Gly	GGG Gly	GAC Asp 310	CGC Arg	CGG Arg	CTG Leu	CTG Leu	CCC Pro 315	GCC Ala	GCG Ala	GTG Val	CAC His	AGC Ser 320	960
	GTG Val	ACG Thr	CTG Leu	CGA Arg	GAG Glu 325	GAG Glu	GAG Glu	GCG Ala	GGC Gly	GCG Ala 330	TAC Tyr	GCG Ala	CCG Pro	CTC Leu	ACG Thr 335	GCG Ala	1008
50	CAC His	GGC Gly	ACC Thr	ATT Ile 340	CTC Leu	ATC Ile	AAC Asn	CGG Arg	GTG Val 345	CTC Leu	GCC Ala	TCG Ser	TGC Cys	TAC Tyr 350	GCT Ala	GTC Val	1056
55	ATC Ile	GAG Glu	GAG Glu 355	CAC His	AGC Ser	TGG Trp	GCA Ala	CAC His 360	CGG Arg	GCC Ala	TTC Phe	GCG Ala	CCT Pro 365	TTC Phe	CGC Arg	CTG Leu	1104
60	GCG Ala	CAC His 370	GCG Ala	CTG Leu	CTG Leu	GCC Ala	GCG Ala 375	CTG Leu	GCA Ala	CCC Pro	GCC Ala 380	CGC Arg	ACG Thr	GAC Asp	GGC Gly	GGG Gly	1152

	GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC	1200
	Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly	
	385 390 395 400	
5	GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC	1248
	Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His	
	405 410 415	
10	ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG	1296
	Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met	
	420 425 430	
15	GCG GTC AAG TCC AGC TG	1313
	Ala Val Lys Ser Ser	
	435	

(2) INFORMATION FOR SEQ ID NO:5:

20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(ix) FEATURE:	
30	(A) NAME/KEY: CDS	
	(B) LOCATION: 1..1257	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
35	ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC	48
	Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser	
	1 5 10 15	
40	TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA	96
	Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
	20 25 30	
45	AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
	35 40 45	
50	CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC	192
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
	50 55 60	
55	AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC	240
	Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
	65 70 75 80	
60	AAT CCC GAC ATT ATC TTT AAG GAT GAG GAG AAC ACG GGA GCG GAC AGG	288
	Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
	85 90 95	
60	CTC ATG ACA CAG AGA TGC AAA GAC AAG CTG AAC TCG CTG GCC ATC TCT	336
	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser	

				100					105					110				
5	GTA Val	ATG Met	AAC Asn 115	CAC His	TGG Trp	CCA Pro	GGG Gly	GTT Val 120	AAG Lys	CTG Leu	CGT Arg	GTG Val	ACA Thr 125	GAG Glu	GGC Gly	TGG Trp	384	
10	GAT Asp	GAG Glu 130	GAC Asp	GGT Gly	CAC His	CAT His	TTT Phe 135	GAA Glu	GAA Glu	TCA Ser	CTC Leu	CAC His 140	TAC Tyr	GAG Glu	GGA Gly	AGA Arg	432	
15	GCT Ala 145	GTT Val	GAT Asp	ATT Ile	ACC Thr	ACC Thr 150	TCT Ser	GAC Asp	CGA Arg	GAC Asp	AAG Lys 155	AGC Ser	AAA Lys	TAC Tyr	GGG Gly	ACA Thr 160	480	
20	CTG Leu	TCT Ser	CGC Arg	CTA Leu 165	GCT Ala	GTG Val	GAG Glu	GCT Ala	GGA Gly	TTT Phe 170	GAC Asp	TGG Trp	GTC Val	TAT Tyr	TAC Tyr 175	GAG Glu	528	
25	TCC Ser	AAA Lys	GCC Ala	CAC His 180	ATT Ile	CAT His	TGC Cys	TCT Ser	GTC Val 185	AAA Lys	GCA Ala	GAA Glu	AAT Asn	TCG Ser 190	GTT Val	GCT Ala	576	
30	GCG Ala	AAA Lys	TCT Ser 195	GGG Gly	GGC Gly	TGT Cys	TTC Phe	CCA Pro 200	GGT Gly	TCG Ser	GCT Ala	CTG Leu	GTC Val 205	TCG Ser	CTC Leu	CAG Gln	624	
35	GAC Asp	GGA Gly 210	GGA Gly	CAG Gln	AAG Lys	GCC Ala	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AAC Asn	CCC Pro 220	GGA Gly	GAC Asp	AAG Lys	GTG Val	672	
40	CTG Leu 225	GCG Ala	GCA Ala	GAC Asp	AGC Ser	GCG Ala 230	GGA Gly	AAC Asn	CTG Leu	GTG Val	TTC Phe 235	AGC Ser	GAC Asp	TTC Phe	ATC Ile	ATG Met 240	720	
45	TTC Phe	ACA Thr	GAC Asp	CGA Arg	GAC Asp 245	TCC Ser	ACG Thr	ACG Thr	CGA Arg	CGT Arg 250	GTG Val	TTT Phe	TAC Tyr	GTC Val	ATA Ile 255	GAA Glu	768	
50	ACG Thr	CAA Gln	GAA Glu	CCC Pro 260	GTT Val	GAA Glu	AAG Lys	ATC Ile	ACC Thr 265	CTC Leu	ACC Thr	GCC Ala	GCT Ala	CAC His	CTC Leu	CTT Leu	816	
55	TTT Phe	GTC Val	CTC Leu	GAC Asp	AAC Asn	TCA Ser	ACG Thr	GAA Glu 280	GAT Asp	CTC Leu	CAC His	ACC Thr	ATG Met 285	ACC Thr	GCC Ala	GCG Ala	864	
60	TAT Tyr	GCC Ala 290	AGC Ser	AGT Ser	GTC Val	AGA Arg	GCC Ala 295	GGA Gly	CAA Gln	AAG Lys	GTG Val	ATG Met 300	GTT Val	GTT Val	GAT Asp	GAT Asp	912	
65	AGC Ser 305	GGT Gly	CAG Gln	CTT Leu	AAA Lys	TCT Ser 310	GTC Val	ATC Ile	GTG Val	CAG Gln 315	CGG Arg	ATA Ile	TAC Tyr	ACG Thr	GAG Glu	GAG Glu 320	960	
70	CAG Gln	CGG Arg	GGC Gly	TCG Ser	TTC Phe 325	GCA Ala	CCA Pro	GTG Val	ACT Thr	GCA Ala 330	CAT His	GGG Gly	ACC Thr	ATT Ile	GTG Val 335	GTC Val	1008	
75	GAC Asp	AGA Arg	ATA Ile	CTG Leu 340	GCG Ala	TCC Ser	TGT Cys	TAC Tyr	GCC Ala 345	GTA Val	ATA Ile	GAG Glu	GAC Asp	CAG Gln	GGG Gly	CTT Leu	1056	

	GCG	CAT	TTG	GCC	TTC	GCG	CCC	GCC	AGG	CTC	TAT	TAT	TAC	GTG	TCA	TCA	1104
	Ala	His	Leu	Ala	Phe	Ala	Pro	Ala	Arg	Leu	Tyr	Tyr	Tyr	Val	Ser	Ser	
			355					360					365				
5	TTC	CTG	TCC	CCC	AAA	ACT	CCA	GCA	GTC	GGT	CCA	ATG	CGA	CTT	TAC	AAC	1152
	Phe	Leu	Ser	Pro	Lys	Thr	Pro	Ala	Val	Gly	Pro	Met	Arg	Leu	Tyr	Asn	
		370					375					380					
10	AGG	AGG	GGG	TCC	ACT	GGT	ACT	CCA	GGC	TCC	TGT	CAT	CAA	ATG	GGA	ACG	1200
	Arg	Arg	Gly	Ser	Thr	Gly	Thr	Pro	Gly	Ser	Cys	His	Gln	Met	Gly	Thr	
	385					390					395				400		
15	TGG	CTT	TTG	GAC	AGC	AAC	ATG	CTT	CAT	CCT	TTG	GGG	ATG	TCA	GTA	AAC	1248
	Trp	Leu	Leu	Asp	Ser	Asn	Met	Leu	His	Pro	Leu	Gly	Met	Ser	Val	Asn	
				405						410					415		
20	TCA	AGC	TG														1256
	Ser	Ser															

(2) INFORMATION FOR SEQ ID NO:6:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: cDNA
- 35 (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1425
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40	ATG	CTG	CTG	CTG	GCG	AGA	TGT	CTG	CTG	CTA	GTC	CTC	GTC	TCC	TCG	CTG	48
	Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu	
	1				5					10				15			
45	CTG	GTA	TGC	TCG	GGA	CTG	GCG	TGC	GGA	CCG	GGC	AGG	GGG	TTC	GGG	AAG	96
	Leu	Val	Cys	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	Lys	
				20				25						30			
50	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCT	TTA	GCC	TAC	AAG	CAG	TTT	ATC	144
	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
			35				40					45					
55	CCC	AAT	GTG	GCC	GAG	AAG	ACC	CTA	GGC	GCC	AGC	GGA	AGG	TAT	GAA	GGG	192
	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	
		50				55					60						
60	AAG	ATC	TCC	AGA	AAC	TCC	GAG	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	TAC	240
	Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65				70					75					80		
	AAC	CCC	GAC	ATC	ATA	TTT	AAG	GAT	GAA	GAA	AAC	ACC	GGA	GCG	GAC	AGG	288

	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
5	CTG Leu	ATG Met	ACT Thr	CAG Gln 100	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys 105	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala 110	ATC Ile	TCG Ser	336
10	GTG Val	ATG Met	AAC Asn 115	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val 120	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr 125	GAG Glu	GGC Gly	TGG Trp	384
15	GAC Asp	GAA Glu 130	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser 135	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His 140	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432
20	GCA Ala 145	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr 150	TCT Ser	GAC Asp	CGC Arg	GAC Asp	CGC Arg 155	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met 160	480
25	CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala 165	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe 170	GAC Asp	TGG Trp	GTG Val	TAC Tyr 175	TAC Tyr 175	GAG Glu	528
30	TCC Ser	AAG Lys	GCA Ala	CAT His 180	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val 185	AAA Lys	GCA Ala	GAG Glu	AAC Asn 190	TCG Ser	GTG Val	GCG Ala	576
35	GCC Ala	AAA Lys	TCG Ser 195	GGA Gly	GGC Gly	TGC Cys	TTC Phe	CCG Pro 200	GGC Gly	TCG Ser	GCC Ala	ACG Thr 205	GTG Val 205	CAC His	CTG Leu	GAG Glu	624
40	CAG Gln	GGC Gly 210	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro 220	GGG Gly	GAC Asp	CGC Arg	GTG Val	672
45	CTG Leu 225	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln 230	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr 235	AGC Ser	GAC Asp	TTC Phe	CTC Leu	ACT Thr 240	720
50	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp 245	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys 250	GTC Val	TTC Phe	TAC Tyr	GTG Val	ATC Ile 255	GAG Glu	768
55	ACG Thr	CGG Arg	GAG Glu	CCG Pro 260	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu 265	CTC Leu	ACC Thr	GCC Ala	GCG Ala	CAC His 270	CTG Leu	CTC Leu	816
60	TTT Phe	GTG Val	GCG Ala 275	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser 280	GCC Ala	ACC Thr	GGG Gly	GAG Glu	CCC Pro 285	GAG Glu	GCG Ala	TCC Ser	864
65	TCG Ser	GGC Gly 290	TCG Ser	GGG Gly	CCG Pro	CCT Pro	TCC Ser 295	GGG Gly	GGC Gly	GCA Ala	CTG Leu	GGG Gly 300	CCT Pro	CGG Arg	GCG Ala	CTG Leu	912
70	TTC Phe 305	GCC Ala	AGC Ser	CGC Arg	GTG Val	CGC Arg 310	CCG Pro	GGC Gly	CAG Gln	CGC Arg	GTG Val 315	TAC Tyr	GTG Val	GTG Val	GCC Ala	GAG Glu 320	960
75	CGT Arg	GAC Asp	GGG Gly	GAC Asp	CGC Arg	CGG Arg	CTC Leu	CTG Leu	CCC Pro	GCC Ala	GCT Ala	GTG Val	CAC His	AGC Ser	GTG Val	ACC Thr	1008

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10      (2) INFORMATION FOR SEQ ID NO:7:
      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1622 base pairs
45      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: both
      (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
50
      (ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 51..1283
55
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
      CATCAGCCCA CCAGGAGACC TCGCCCGCCG CTCCCCGGG CTCCCCGGCC ATG TCT
60                                     Met Ser
                                     1

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	GTG	CTC	ATT	TTC	CTG	GAC	CGC	GAG	CCC	CAC	AGG	CTG	AGA	GCC	TTC	CAG	824
	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln	
			245					250					255				
5	GTC	ATC	GAG	ACT	CAG	GAC	CCC	CCA	CGC	CGC	CTG	GCA	CTC	ACA	CCC	GCT	872
	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
		260					265					270					
10	CAC	CTG	CTC	TTT	ACG	GCT	GAC	AAT	CAC	ACG	GAG	CCG	GCA	GCC	CGC	TTC	920
	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe	
	275					280					285					290	
15	CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG	968
	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
					295					300					305		
20	GCT	GGG	GTG	CCA	GGC	CTG	CAG	CCT	GCC	CGC	GTG	GCA	GCT	GTC	TCT	ACA	1016
	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr	
				310					315					320			
25	CAC	GTG	GCC	CTC	GGG	GCC	TAC	GCC	CCG	CTC	ACA	AAG	CAT	GGG	ACA	CTG	1064
	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu	
			325					330					335				
30	GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC	1112
	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
		340					345					350					
35	CAC	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	AGA	CTC	TTT	CAC	AGC	TTG	1160
	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
	355				360						365					370	
40	GCA	TGG	GGC	AGC	TGG	ACC	CCG	GGG	GAG	GGT	GTG	CAT	TGG	TAC	CCC	CAG	1208
	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
				375					380						385		
45	CTG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	CTG	CTA	GAA	GAG	GGC	AGC	TTC	CAC	1256
	Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
				390				395					400				
50	CCA	CTG	GGC	ATG	TCC	GGG	GCA	GGG	AGC	TGAAAGGACT	CCACCGCTGC						1303
	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser								
		405					410										
55	CCTCCTGGAA	CTGCTGTACT	GGGTCCAGAA	GCCTCTCAGC	CAGGAGGGAG	CTGGCCCTGG											1363
	AAGGGACCTG	AGCTGGGGGA	CACTGGCTCC	TGCCATCTCC	TCTGCCATGA	AGATACACCA											1423
	TTGAGACTTG	ACTGGGCAAC	ACCAGCGTCC	CCCACCCGCG	TCGTGGTGTA	GTCATAGAGC											1483
	TGCAAGCTGA	GCTGGCGAGG	GGATGGTTGT	TGACCCCTCT	CTCCTAGAGA	CCTTGAGGCT											1543
	GGCACGGCGA	CTCCCAACTC	AGCCTGCTCT	CACTACGAGT	TTTCATACTC	TGCCTCCCCC											1603
	ATTGGGAGGG	CCCATTTCCC															1622

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15	ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG	48
	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
20	GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG	96
	Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
	20 25 30	
25	CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT	144
	Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
	35 40 45	
30	GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG	192
	Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
	50 55 60	
35	GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC	240
	Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
	65 70 75 80	
40	TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC	288
	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
	85 90 95	
45	CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT	336
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
	100 105 110	
50	GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
55	TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
	130 135 140	
60	CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG	480
	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
	145 150 155 160	
65	TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
	165 170 175	
70	GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
	Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
	180 185 190	

	GCG Ala	GTC Val	CGG Arg 195	GCG Ala	GGC Gly	GGC Gly	TGC Cys	TTT Phe 200	CCG Pro	GGA Gly	AAT Asn	GCA Ala	ACT Thr 205	GTG Val	CGC Arg	CTG Leu	624
5	TGG Trp 210	AGC Ser	GGC Gly	GAG Glu	CGG Arg	AAA Lys	GGG Gly 215	CTG Leu	CGG Arg	GAA Glu	CTG Leu	CAC His 220	CGC Arg	GGA Gly	GAC Asp	TGG Trp	672
10	GTT Val 225	TTG Leu	GCG Ala	GCC Ala	GAT Asp	GCG Ala 230	TCA Ser	GGC Gly	CGG Arg	GTG Val	GTG Val 235	CCC Pro	ACG Thr	CCG Pro	GTG Val	CTG Leu 240	720
15	CTC Leu	TTC Phe	CTG Leu	GAC Asp	CGG Arg 245	GAC Asp	TTG Leu	CAG Gln	CGC Arg	CGG Arg 250	GCT Ala	TCA Ser	TTT Phe	GTG Val	GCT Ala 255	GTG Val	768
20	GAG Glu	ACC Thr	GAG Glu	TGG Trp 260	CCT Pro	CCA Pro	CGC Arg	AAA Lys	CTG Leu 265	TTG Leu	CTC Leu	ACG Thr	CCC Pro	TGG Trp 270	CAC His	CTG Leu	816
	GTG Val	TTT Phe	GCC Ala 275	GCT Ala	CGA Arg	GGG Gly	CCG Pro	GCG Ala 280	CCC Pro	GCG Ala	CCA Pro	GGC Gly	GAC Asp 285	TTT Phe	GCA Ala	CCG Pro	864
25	GTG Val	TTC Phe 290	GCG Ala	CGC Arg	CGG Arg	CTA Leu	CGC Arg 295	GCT Ala	GGG Gly	GAC Asp	TCG Ser	GTG Val 300	CTG Leu	GCG Ala	CCC Pro	GGC Gly	912
30	GGG Gly 305	GAT Asp	GCG Ala	CTT Leu	CGG Arg	CCA Pro 310	GCG Ala	CGC Arg	GTG Val	GCC Ala	CGT Arg 315	GTG Val	GCG Ala	CGG Arg	GAG Glu	GAA Glu 320	960
35	GCC Ala	GTG Val	GGC Gly	GTG Val	TTC Phe 325	GCG Ala	CCG Pro	CTC Leu	ACC Thr	GCG Ala 330	CAC His	GGG Gly	ACG Thr	CTG Leu	CTG Leu 335	GTG Val	1008
40	AAC Asn	GAT Asp	GTC Val 340	CTG Leu	GCC Ala	TCT Ser	TGC Cys	TAC Tyr	GCG Ala 345	GTT Val	CTG Leu	GAG Glu	AGT Ser	CAC His 350	CAG Gln	TGG Trp	1056
	GCG Ala	CAC His	CGC Arg 355	GCT Ala	TTT Phe	GCC Ala	CCC Pro	TTG Leu 360	AGA Arg	CTG Leu	CTG Leu	CAC His	GCG Ala 365	CTA Leu	GGG Gly	GCG Ala	1104
45	CTG Leu	CTC Leu 370	CCC Pro	GGC Gly	GGG Gly	GCC Ala	GTC Val 375	CAG Gln	CCG Pro	ACT Thr	GGC Gly	ATG Met 380	CAT His	TGG Trp	TAC Tyr	TCT Ser	1152
50	CGG Arg 385	CTC Leu	CTC Leu	TAC Tyr	CGC Arg	TTA Leu 390	GCG Ala	GAG Glu	GAG Glu	CTA Leu	CTG Leu 395	GGC Gly	TG				1191
55	(2) INFORMATION FOR SEQ ID NO:9:																
	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 1251 base pairs																
	(B) TYPE: nucleic acid																
60	(C) STRANDEDNESS: both																
	(D) TOPOLOGY: linear																

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1248

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC	48
	Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	
	1 5 10 15	
15	AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT	96
	Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
	20 25 30	
20	TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG	144
	Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
25	CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	
	50 55 60	
30	TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	
	65 70 75 80	
35	CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	
	85 90 95	
40	GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG	336
	Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	
	100 105 110	
45	GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT	384
	Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	
50	GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT	432
	Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	
	130 135 140	
55	GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
	145 150 155 160	
60	TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC	528
	Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
	165 170 175	
65	TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT	576
	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
	180 185 190	
70	TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG	624
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	

1248

	195	200	205	
5	ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220			672
10	GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235 240			720
	TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255			768
15	GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270			816
20	CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275 280 285			864
25	ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290 295 300			912
30	GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305 310 315 320			960
	GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325 330 335			1008
35	ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340 345 350			1056
40	AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355 360 365			1104
45	ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu 370 375 380			1152
50	GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp 385 390 395 400			1200
	CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser 405 410 415			1248
55	TGA			1251

(2) INFORMATION FOR SEQ ID NO:10:

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5	Met	Val	Glu	Met	Leu	Leu	Leu	Thr	Arg	Ile	Leu	Leu	Val	Gly	Phe	Ile
10	1				5					10					15	
	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly
				20					25					30		
15	Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys
			35					40					45			
	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg
		50					55					60				
20	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr
	65					70					75					80
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly
25					85					90					95	
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu
				100					105					110		
30	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr
			115					120					125			
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr
		130					135					140				
35	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys
	145					150					155					160
	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val
40				165						170					175	
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn
			180						185					190		
45	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val
			195					200					205			
	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly
		210					215					220				
50	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp
	225					230					235					240
	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr
55				245						250					255	
	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala
			260						265					270		
60	His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly
		275						280					285			

Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300

5 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320

Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335

10 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350

15 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365

Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380

20 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400

Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415

25 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

30 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

55 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

60 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile

TOUCHDOWN

	100					105					110					
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
			115					120					125			
5	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
		130					135					140				
10	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145					150					155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
15	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
			195					200					205			
20	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
			210				215					220				
	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
25	225					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245						250					255	
30	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
			275					280					285			
35	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
		290					295				300					
	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
40	305					310					315					320
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
					325					330					335	
45	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp
				340					345					350		
	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala
			355					360					365			
50	Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser
		370					375				380					
	Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly				
55	385					390					395					

(2) INFORMATION FOR SEQ ID NO:12:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10	Met	Ser	Pro	Ala	Trp	Leu	Arg	Pro	Arg	Leu	Arg	Phe	Cys	Leu	Phe	Leu
	1				5					10					15	
	Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg
				20					25					30		
15	Val	Val	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala
			35					40					45			
20	Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser
		50					55					60				
	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu
	65					70					75					80
25	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn
					85					90					95	
	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn
				100					105					110		
30	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg
			115					120					125			
35	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu
		130					135					140				
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg
	145					150					155					160
40	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp
					165					170					175	
	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser
				180					185					190		
45	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala
			195					200					205			
50	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys
		210					215					220				
	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe
	225					230					235					240
55	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala
					245					250					255	
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr
				260					265					270		
60	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala

TOPOL=0123456789

	275	280	285
5	His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val 290 295 300		
	Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val 305 310 315 320		
10	Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly 325 330 335		
	Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 340 345 350		
15	Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro 355 360 365		
	Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr 370 375 380		
20	Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr 385 390 395 400		
	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Leu	Leu	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Val	Ile	Leu	Ala	Ser	Ser
1				5					10					15	
Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly
		20						25					30		
Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe
		35					40					45			
Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu
		50				55					60				
Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn
	65				70					75					80
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp
			85						90					95	
Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile
		100						105					110		

	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
			115					120					125			
5	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly
		130					135					140				
	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly
10	145					150					155					160
	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val
15				180					185					190		
	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu
			195					200					205			
20	Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg
		210					215					220				
	Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu
25	225					230					235					240
	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile
					245					250					255	
	Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu
30				260					265					270		
	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser
			275					280					285			
35	Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val
		290					295					300				
	Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser
40	305					310					315					320
	Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala
					325				330						335	
	His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val
45				340					345					350		
	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu
			355					360					365			
50	Ala	His	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly
		370					375					380				
	Gly	Gly	Gly	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly
55	385					390					395					400
	Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His
					405					410					415	
	Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met
60				420					425					430		

Ala Val Lys Ser Ser
435

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Arg	Leu	Leu	Thr	Arg	Val	Leu	Leu	Val	Ser	Leu	Leu	Thr	Leu	Ser	1	5	10	15
Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg	20	25	30	
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	35	40	45	
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	50	55	60	
Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	65	70	75	80
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	85	90	95	
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	100	105	110	
Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	115	120	125	
Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	130	135	140	
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	145	150	155	160
Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	165	170	175	
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	180	185	190	
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln	195	200	205	
Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	210	215	220	
Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met	225	230	235	240

	50					55					60						
5	Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80	
	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
10	Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser	
	Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp	
15	Asp	Glu 130	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg	
	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160	
20	Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu	
25	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala	
	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe	Pro 200	Gly	Ser	Ala	Thr	Val 205	His	Leu	Glu	
30	Gln	Gly 210	Gly	Thr	Lys	Leu	Val 215	Lys	Asp	Leu	Ser	Pro 220	Gly	Asp	Arg	Val	
	Leu 225	Ala	Ala	Asp	Asp	Gln 230	Gly	Arg	Leu	Leu	Tyr 235	Ser	Asp	Phe	Leu	Thr 240	
35	Phe	Leu	Asp	Arg	Asp 245	Asp	Gly	Ala	Lys	Lys 250	Val	Phe	Tyr	Val	Ile 255	Glu	
40	Thr	Arg	Glu	Pro 260	Arg	Glu	Arg	Leu	Leu 265	Leu	Thr	Ala	Ala	His 270	Leu	Leu	
	Phe	Val	Ala 275	Pro	His	Asn	Asp	Ser 280	Ala	Thr	Gly	Glu	Pro 285	Glu	Ala	Ser	
45	Ser	Gly 290	Ser	Gly	Pro	Pro	Ser 295	Gly	Gly	Ala	Leu	Gly 300	Pro	Arg	Ala	Leu	
	Phe 305	Ala	Ser	Arg	Val	Arg 310	Pro	Gly	Gln	Arg	Val 315	Tyr	Val	Val	Ala	Glu 320	
50	Arg	Asp	Gly	Asp	Arg 325	Arg	Leu	Leu	Pro	Ala 330	Ala	Val	His	Ser	Val 335	Thr	
55	Leu	Ser	Glu	Glu 340	Ala	Ala	Gly	Ala	Tyr 345	Ala	Pro	Leu	Thr	Ala 350	Gln	Gly	
	Thr	Ile	Leu 355	Ile	Asn	Arg	Val	Leu 360	Ala	Ser	Cys	Tyr	Ala 365	Val	Ile	Glu	
60	Glu	His 370	Ser	Trp	Ala	His	Arg 375	Ala	Phe	Ala	Pro	Phe 380	Arg	Leu	Ala	His	

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
385 390 395 400

5 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
420 425 430

10 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
435 440 445

15 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
450 455 460

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465 470 475

20 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

55 Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

60 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp

Topol = 0 F 2 3 5 0

	165	170	175
5	Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser 180 185 190		
	Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala 195 200 205		
10	Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg 210 215 220		
	Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe 225 230 235 240		
15	Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala 245 250 255		
	Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr 260 265 270		
20	Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala 275 280 285		
25	Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val 290 295 300		
	Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val 305 310 315 320		
30	Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly 325 330 335		
	Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 340 345 350		
35	Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His 355 360 365		
40	Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr 370 375 380		
	Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser 385 390 395 400		
45	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410		

(2) INFORMATION FOR SEQ ID NO:17:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

60	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
	1 5 10 15

	Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
5	Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
		50					55					60				
10	Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70				75						80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
15	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
			100						105					110		
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
20			115					120					125			
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
		130					135					140				
25	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145					150					155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
30	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
35			195					200					205			
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
		210					215					220				
40	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
	225					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
					245					250					255	
45	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
50			275					280					285			
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
		290					295					300				
55	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
	305					310					315					320
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
					325					330					335	
60	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp

340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

5 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

10 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

25 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

40 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

45 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145 150 155 160

55 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
180 185 190

60 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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	Met 1	Asp	Asn	His	Ser 5	Ser	Val	Pro	Trp	Ala 10	Ser	Ala	Ala	Ser	Val 15	Thr	
5	TGT Cys	CTC Leu	TCC Ser	CTG Leu 20	GGA Gly	TGC Cys	CAA Gln	ATG Met	CCA Pro 25	CAG Gln	TTC Phe	CAG Gln	TTC Phe	CAG Gln 30	TTC Phe	CAG Gln	96
10	CTC Leu	CAA Gln	ATC Ile 35	CGC Arg	AGC Ser	GAG Glu	CTC Leu	CAT His 40	CTC Leu	CGC Arg	AAG Lys	CCC Pro	GCA Ala 45	AGA Arg	AGA Arg	ACG Thr	144
15	CAA Gln 50	ACG Thr	ATG Met	CGC Arg	CAC His	ATT Ile	GCG Ala 55	CAT His	ACG Thr	CAG Gln	CGT Arg	TGC Cys 60	CTC Leu	AGC Ser	AGG Arg	CTG Leu	192
20	ACC Thr 65	TCT Ser	CTG Leu	GTG Val	GCC Ala	CTG Leu 70	CTG Leu	CTG Leu	ATC Ile	GTC Val	TTG Leu 75	CCG Pro	ATG Met	GTC Val	TTT Phe	AGC Ser 80	240
25	CCG Pro	GCT Ala	CAC His	AGC Ser	TGC Cys 85	GGT Gly	CCT Pro	GGC Gly	CGA Arg	GGA Gly 90	TTG Leu	GGT Gly	CGT Arg	CAT His	AGG Arg 95	GCG Ala	288
30	CGC Arg	AAC Asn	CTG Leu	TAT Tyr 100	CCG Pro	CTG Leu	GTC Val	CTC Leu	AAG Lys 105	CAG Gln	ACA Thr	ATT Ile	CCC Pro	AAT Asn 110	CTA Leu	TCC Ser	336
35	GAG Glu	TAC Tyr	ACG Thr 115	AAC Asn	AGC Ser	GCC Ala	TCC Ser	GGA Gly 120	CCT Pro	CTG Leu	GAG Glu	GGT Gly 125	GTG Val	ATC Ile	CGT Arg	CGG Arg	384
40	GAT Asp 130	TCG Ser	CCC Pro	AAA Lys	TTC Phe	AAG Lys	GAC Asp 135	CTC Leu	GTG Val	CCC Pro	AAC Asn	TAC Tyr 140	AAC Asn	AGG Arg	GAC Asp	ATC Ile	432
45	CTT Leu 145	TTC Phe	CGT Arg	GAC Asp	GAG Glu	GAA Glu 150	GGC Gly	ACC Thr	GGA Gly	GCG Ala	GAT Asp 155	GGC Gly	TTG Leu	ATG Met	AGC Ser	AAG Lys 160	480
50	CGC Arg	TGC Cys	AAG Lys	GAG Glu 165	AAG Lys	CTA Leu	AAC Asn	GTG Val	CTG Leu	GCC Ala 170	TAC Tyr	TCG Ser	GTG Val	ATG Met	AAC Asn 175	GAA Glu	528
55	TGG Trp	CCC Pro	GGC Gly 180	ATC Ile	CGG Arg	CTG Leu	CTG Leu	GTC Val	ACC Thr 185	GAG Glu	AGC Ser	TGG Trp	GAC Asp	GAG Glu 190	GAC Asp	TAC Tyr	576
60	CAT His	CAC His	GGC Gly 195	CAG Gln	GAG Glu	TCG Ser	CTC Leu	CAC His 200	TAC Tyr	GAG Glu	GGC Gly	CGA Arg	GCG Ala 205	GTG Val	ACC Thr	ATT Ile	624
65	GCC Ala 210	ACC Thr	TCC Ser	GAT Asp	CGC Arg	GAC Asp	CAG Gln 215	TCC Ser	AAA Lys	TAC Tyr	GGC Gly 220	ATG Met	CTC Leu	GCT Ala	CGC Arg	CTG Leu	672
70	GCC Ala 225	GTC Val	GAG Glu	GCT Ala	GGA Gly	TTC Phe 230	GAT Asp	TGG Trp	GTC Val	TCC Ser	TAC Tyr 235	GTC Val	AGC Ser	AGG Arg	CGC Arg	CAC His 240	720
75	ATC Ile	TAC Tyr	TGC Cys	TCC Ser	GTC Val	AAG Lys	TCA Ser	GAT Asp	TCG Ser	TCG Ser	ATC Ile	AGT Ser	TCC Ser	CAC His	GTG Val	CAC His	768

TABLE 10-10-10

255

[illegible]

60 (2) INFORMATION FOR SEQ ID NO:20:

(A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

10	Met 1	Asp	Asn	His	Ser 5	Ser	Val	Pro	Trp	Ala 10	Ser	Ala	Ala	Ser	Val	Thr
	Cys	Leu	Ser	Leu 20	Gly	Cys	Gln	Met	Pro 25	Gln	Phe	Gln	Phe	Gln 30	Phe	Gln
15	Leu	Gln	Ile 35	Arg	Ser	Glu	Leu	His 40	Leu	Arg	Lys	Pro 45	Ala	Arg	Arg	Thr
	Gln	Thr 50	Met	Arg	His	Ile	Ala 55	His	Thr	Gln	Arg	Cys 60	Leu	Ser	Arg	Leu
20	Thr 65	Ser	Leu	Val	Ala	Leu 70	Leu	Leu	Ile	Val	Leu 75	Pro	Met	Val	Phe	Ser 80
	Pro	Ala	His	Ser	Cys 85	Gly	Pro	Gly	Arg	Gly 90	Leu	Gly	Arg	His	Arg 95	Ala
25	Arg	Asn	Leu 100	Tyr	Pro	Leu	Val	Leu	Lys 105	Gln	Thr	Ile	Pro	Asn 110	Leu	Ser
30	Glu	Tyr	Thr 115	Asn	Ser	Ala	Ser	Gly 120	Pro	Leu	Glu	Gly	Val 125	Ile	Arg	Arg
	Asp	Ser 130	Pro	Lys	Phe	Lys	Asp 135	Leu	Val	Pro	Asn	Tyr 140	Asn	Arg	Asp	Ile
35	Leu 145	Phe	Arg	Asp	Glu	Glu 150	Gly	Thr	Gly	Ala	Asp 155	Gly	Leu	Met	Ser	Lys 160
40	Arg	Cys	Lys	Glu	Lys 165	Leu	Asn	Val	Leu	Ala 170	Tyr	Ser	Val	Met	Asn 175	Glu
	Trp	Pro	Gly	Ile 180	Arg	Leu	Leu	Val	Thr 185	Glu	Ser	Trp	Asp	Glu 190	Asp	Tyr
45	His	His	Gly 195	Gln	Glu	Ser	Leu	His 200	Tyr	Glu	Gly	Arg	Ala 205	Val	Thr	Ile
	Ala	Thr 210	Ser	Asp	Arg	Asp	Gln 215	Ser	Lys	Tyr	Gly	Met 220	Leu	Ala	Arg	Leu
50	Ala 225	Val	Glu	Ala	Gly	Phe 230	Asp	Trp	Val	Ser	Tyr 235	Val	Ser	Arg	Arg	His 240
55	Ile	Tyr	Cys	Ser	Val 245	Lys	Ser	Asp	Ser	Ser 250	Ile	Ser	Ser	His	Val 255	His
	Gly	Cys	Phe	Thr 260	Pro	Glu	Ser	Thr	Ala 265	Leu	Leu	Glu	Ser	Gly 270	Val	Arg
60	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr

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	275	280	285
5	Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg 290 295 300		
	Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly 305 310 315 320		
10	Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro 325 330 335		
	Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys 340 345 350		
15	Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln 355 360 365		
	Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro 370 375 380		
20	Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys 385 390 395 400		
25	Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro 405 410 415		
	Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln 420 425 430		
30	Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly 435 440 445		
	Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu 450 455 460		
35	Pro Gln Ser Trp Arg His Asp 465 470		
40	(2) INFORMATION FOR SEQ ID NO:21:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 221 amino acids		
	(B) TYPE: amino acid		
	(D) TOPOLOGY: linear		
45	(ii) MOLECULE TYPE: peptide		
	(v) FRAGMENT TYPE: internal		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:		
55	Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu 1 5 10 15		
	Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr 20 25 30		
60	Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu 35 40 45		

	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50						55					60				
5	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
	65					70					75					80
	Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
				85						90					95	
10	Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
				100					105					110		
	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
15			115					120					125			
	Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
		130					135					140				
20	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
	145					150					155					160
	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
					165					170					175	
25	Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
				180					185					190		
	Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
30			195					200					205			
	Xaa	Leu	Xaa	Xaa	Ser	Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Arg			
		210					215					220				

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Xaa	Xaa	Arg	Arg	Xaa	Xaa	Xaa	Pro	Lys
	1				5					10					15	
	Xaa	Leu	Xaa	Pro	Leu	Xaa	Tyr	Lys	Gln	Phe	Xaa	Pro	Xaa	Xaa	Xaa	Glu
				20					25					30		
	Xaa	Thr	Leu	Gly	Ala	Ser	Gly	Xaa	Xaa	Glu	Gly	Xaa	Xaa	Xaa	Arg	Xaa
			35				40						45			
60	Ser	Glu	Arg	Phe	Xaa	Xaa	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile
		50					55					60				

	Phe	Lys	Asp	Glu	Glu	Asn	Xaa	Gly	Ala	Asp	Arg	Leu	Met	Thr	Xaa	Arg
	65					70					75					80
5	Cys	Lys	Xaa	Xaa	Xaa	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp
					85					90					95	
	Pro	Gly	Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Xaa	Asp	Glu	Asp	Gly	His
				100					105					110		
10	His	Xaa	Xaa	Xaa	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Xaa	Asp	Ile	Thr
			115					120					125			
	Thr	Ser	Asp	Arg	Asp	Xaa	Xaa	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala
15		130					135					140				
	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Xaa	Xaa	His	Xaa
	145					150					155					160
20	His	Xaa	Ser	Val	Lys	Xaa	Xaa									
					165											

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